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1644

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/442,143

DATE: 03/08/2000
TIME: 04:40:44

INPUT SET: S34972.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

4 1/2

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Levy, Gary
6 Clark, David A.
7
8 (ii) TITLE OF INVENTION: Methods of Modulating Immune Coagulation
9
10 (iii) NUMBER OF SEQUENCES: 4
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: BERESKIN & PARR
14 (B) STREET: 40 King Street West
15 (C) CITY: Toronto
16 (D) STATE: Ontario
17 (E) COUNTRY: Canada
18 (F) ZIP: M5H 3Y3
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: 09/442,143
28 (B) FILING DATE: 15-NOV-1999
29 (C) CLASSIFICATION:
30
31 (viii) ATTORNEY/AGENT INFORMATION:
32 (A) NAME: Gravelle, Micheline
33 (B) REGISTRATION NUMBER: 40,261
34 (C) REFERENCE/DOCKET NUMBER: 9579-014
35
36 (ix) TELECOMMUNICATION INFORMATION:
37 (A) TELEPHONE: (416) 364-7311
38 (B) TELEFAX: (416) 361-1398
39
40
41 (2) INFORMATION FOR SEQ ID NO:1:
42
43 (i) SEQUENCE CHARACTERISTICS:
44 (A) LENGTH: 4630 base pairs
45 (B) TYPE: nucleic acid
46 (C) STRANDEDNESS: single

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TC 1600 MAIL ROOM

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/442,143DATE: 03/08/2000
TIME: 04:40:45

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

47	GATCTAGGGT	TGGAAGCCAG	GTCTCCTGAG	TATGCGAGAA	TAAATACAGT	CATGGAAGTG	60
48							
49	TAAAGAGTCT	GCCAACATTT	TGAGAATGTG	AATAGGATTT	GGCTAAAATT	AAGGGGATAT	120
50							
51	ACAGAAAAGT	CATAGGAAAT	CAGGTAAAG	ACATAAATAT	GAGATAGGCT	ACAGAGTGTT	180
52							
53	TTAAGTAATA	CAATAAAACA	TTTAGATTTT	TGCCCATGTC	AGTCATTTTG	AAATTATTTT	240
54							
55	TAAAGCAAAA	AAACCCTTTT	TAAACAAGAA	ATCTTATGAG	ATGTCAATAT	GCAAAACAAA	300
56							
57	TTAAAAGGAG	GTGGTTTCTC	TAAGTGAAGC	TGTTCTCTCT	TCCTGCCTTC	AGCCTCTGAA	360
58							
59	GAGAAAGTTA	GAAAACATTT	ATCATTAAATG	CTACATGTTT	TGAACAAGCT	GATATACCAA	420
60							
61	GTGGCCCAGA	GAGCAGGTAG	AAGAACCAGC	GTGGAGACAG	AAAGCAAGAG	GCCCGCCTGC	480
62							
63	CAGGGCTACC	TGCAGAAAGA	AAGGGCAAAG	ATGCTGTAGG	CAAGAGAAGT	TCAGGACAGA	540
64							
65	CAC'TGGCATA	GCTCAAAGAT	TCACATTTGA	GCAGCTGTGG	AAGATGACAG	TACAATTACC	600
66							
67	AAAATGTGCA	AGGGCAAAGG	AGGCAGCTAC	TGGTTTTGAT	GAAAGACAAT	TATGTCCTTT	660
68							
69	TAAATGGGTC	TTAGACATTT	AGACATTTAT	ATACACTATG	CTACGGACAA	AGGAATAGAA	720
70							
71	AGTAGCACTT	TTTTCTCCAC	TAGTTTTCTT	CTCTTTTTCA	AGTAGATGAA	GCAAAAGTCA	780
72							
73	ACTGCAATAG	TCAGAAAGCT	GTACTTTGTT	ACACTTAGAA	ACTTCTAAAA	GTGCTTAAGA	840
74							
75	TTTCACCTGA	AAGTCCAACA	TGAAGAAAAT	ACAGGCTCCC	CAATGCCCCA	TTCTAAGAAG	900
76							
77	GAAAAAGGAC	CATTTTCATT	TTAGTAACGT	TTCTGTTCTA	TAGACAGTTT	GGATAACTAG	960
78							
79	CTCTTACTTT	TTATCTTTAA	AAACTGTTTT	TCCAGTGAAG	TTACGTATAA	TTATTTACTT	1020
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81	CAAGCGTAGT	ATACCAAATT	ACTTTAGAAA	TGCAAGACTT	TTCTTATACT	TCATAAAATA	1080
82							
83	CATTATGAAA	GTGAATCTTG	TTGGCTGTGT	ACATTTGACT	ATAATAATTT	CAATGCATAT	1140
84							
85	TATTTCTATT	GAGAGTAAGT	TACAGTTTTT	GGCAAACGTC	GTTTGATGAG	GGCTATCTCC	1200
86							
87	TCTTCCTGTG	CGTTTCTAAA	ACTTGTGATG	CAAACGCTCC	CACCC'TTTC	TGGGAACACA	1260
88							
89	GAAAGCCTGA	CTCAGGCCAT	GGCCGCTATT	AAAGCAGCTC	CAGCCCTGCG	CACTCCCTGC	1320
90							
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100	TGGGGTGAGC	AGCACTGTAA	AGATGAAGCT	GGCTAACTGG	TACTGGCTGA	GCTCAGCTGT	1380
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102	TCTTGCCACT	TACGGTTTTT	TGGTTGTGGC	AAACAATGAA	ACAGAGGAAA	TTAAAGATGA	1440
103							
104	AAGAGCAAAG	GATGTCTGCC	CAGTGAGACT	AGAAAGCAGA	GGGAAATGCG	AAGAGGCAGG	1500
105							
106	GGAGTGCCCC	TACCAGGTAA	GCCTGCCCCC	CTTGACTATT	CAGCTCCCGA	AGCAATTCAG	1560
107							
108	CAGGATCGAG	GAGGTGTTCA	AAGAAGTCCA	AAACCTCAAG	GAAATCGTAA	ATAGTCTAAA	1620
109							
110	GAAATCTTGC	CAAGACTGCA	AGCTGCAGGC	TGATGACAAC	GGAGACCCAG	GCAGAAACGG	1680
111							
112	ACTGTTGTTA	CCCAGTACAG	GAGCCCCGGG	AGAGGTTGGT	GATAACAGAG	TTAGAGAATT	1740
113							
114	AGAGAGTGAG	GTTAACAAGC	TGTCCTCTGA	GCTAAAGAAT	GCCAAAGAGG	AGATCAATGT	1800
115							
116	ACTTCATGGT	CGCCTGGAGA	AGCTGAATCT	TGTAAATATG	AACAACATAG	AAAATTATGT	1860
117							
118	TGACAGCAAA	GTGGCAAATC	TAACATTTGT	TGTCAATAGT	TTGGATGGCA	AATGTTCAAA	1920
119							
120	GTGTCCCAGC	CAAGAACAAA	TACAGTCACG	TCCAGGTATG	TATAATAATG	TTTTCTTATC	1980
121							
122	ATATGTTTCAT	AAATGTTATA	CAGTCAGAGA	TGTATCTAAA	AGATTAACCT	GAGTCAGTAA	2040
123							
124	GTAAATAGA	TGACAGATTA	AGTCTTTTAT	TTATCAAGGT	GCACAGGAAA	AAATAAATAT	2100
125							
126	CTTCTCAAAT	ATGACCACAT	AAATATGACC	TAATTACAAA	ATCATAGTTA	GTTCTGTATC	2160
127							
128	CAC TGGAAGT	CAC TTTCAAT	TTTAAGATCT	TATTTGTTAA	TGCCAGACCT	ACTTGCAAGC	2220
129							
130	AGAGATTAGA	GGTCCTTTTCT	GCTTTTATAAC	ATTAGGTTCT	TCTTGTGAGG	CCTTAAGCAT	2280
131							
132	TTACTAAACA	CCTTCAAGTA	AGTTTAGTAA	AGTTTCATTA	CTGCCATTGA	TTCAATTATC	2340
133							
134	AAACTGCCTT	TGTACATATA	AAGAATTCTT	CAGATGCATG	GTTTCTATTA	ACAAGATCCA	2400
135							
136	ATGCCCTTCCT	TTTATTTCCC	CTTCAGTTCA	ACATCTAATA	TATAAAGATT	GCTCTGACTA	2460
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138	CTACGCAATA	GGCAAAAGAA	GCAGTGAGAC	CTACAGAGTT	ACACCTGATC	CCAAAAATAG	2520
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140	TAGCTTTGAA	GTTTACTGTG	ACATGGAGAC	CATGGGGGGA	GGCTGGACAG	TGCTGCAGGC	2580
141							
142	ACGTCTCGAT	GGGAGCACCA	ACTTCACCAG	AACATGGCAA	GACTACAAAG	CAGGCTTTGG	2640
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144	AAACCTCAGA	AGGGAATTTT	GGCTGGGGAA	CGATAAAATT	CATCTTCTGA	CCAAGAGTAA	2700
145							
146	GGAAATGATT	CTGAGAATAG	ATCTTGAAGA	CTTTAATGGT	GTCGAAC'TAT	ATGCC'TTGTA	2760
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148	TGATCAGTTT	TATGTGGCTA	ATGAGTTTCT	CAAATATCGT	TTACACGTTG	GTAAC'TATAA	2820
149							
150	TGGCACAGCT	GGAGATGCAT	TACGTTTCAA	CAAACATTAC	AACCACGATC	TGAAG'TTTTT	2880
151							
152	CACCACTCCA	GATAAAGACA	ATGATCGATA	TCCTTCTGGG	AACTGTGGGC	TGTACTACAG	2940

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154	TTCAGGCTGG	TGGTTTGATG	CATGTCTTTC	TGCAAACTTA	AATGGCAAAT	ATTATCACCA	3000
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156	AAAATACAGA	GGTGTCCGTA	ATGGGATTTT	CTGGGGTACC	TGGCCTGGTG	TAAGTGAGGC	3060
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158	ACACCCTGGT	GGCTACAAGT	CCTCCTTCAA	AGAGGCTAAG	ATGATGATCA	GACCCAAGCA	3120
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160	CTTTAAGCCA	TAAATCACTC	TGTTCAATTCC	TCCAGGTATT	CGTTATCTAA	TAGGGCAATT	3180
161							
162	AATTCCTTGT	TTCATATTTT	TCATAGCTAA	AAAATGATGT	CTGACGGCTA	GGTTCTTATG	3240
163							
164	CTACACAGCA	TTTGAAATAA	AGCTGAAAAA	CAATGCATTT	TAAAGGAGTC	CTTTGTTGTT	3300
165							
166	ATGCTGTTAT	CCAATGAACA	CTTGCAAGCA	ATTAGCAATA	TTGAGAATTA	TACATTAGAT	3360
167							
168	TTACAATTCT	TTTAATTTCT	ATTGAAACTT	TTTCTATTGC	TTGTATTACT	TGCTGTATTT	3420
169							
170	AAAAAATAAT	TGTTGGCTGG	GTGTGGTAGC	TCACGCCTGT	AATCCCAGCA	CTTTGGAATG	3480
171							
172	TCAAGGCAGG	CAGATCACTT	GAGGTCAGGA	GTTTGAGACC	AGCCTGGCCA	AACATGTGAA	3540
173							
174	ACGCTGTCTC	TATTA AAAAT	ACAAAAATTA	GCCGGGCATG	GTGGTACATG	CCTGTAATCA	3600
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176	ACGCTGTTTA	TTAAAAATAC	AAAAATTAGC	CGGGCATGGT	GGACATGCCT	GTAATCCTAG	3660
177							
178	TACTTGGGAG	GCTGAGGCAG	GAGAATCGCT	TGAACCTGAG	AGGAAGAGGT	TGCAGTGAGC	3720
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180	CAAGAATGAG	CCACTGCACT	CCAGCATGGG	TGACAGAGAA	AACTCTGTCT	CAAACAAAAA	3780
181							
182	AATAATAAAA	TTTATTTCAGT	AGGTGGATTTC	TACACAAAGT	AATCTGTATT	TGGGCCATGA	3840
183							
184	TTTAAGCACA	TCTGAAGGTA	TATCACTCTT	TTCAGGCTAT	AATTATTTGG	GTAATCTTCA	3900
185							
186	TTCTGAGACA	AACTTAATCT	ATATCATTTA	CTTTGCAACA	GAACAACCCCT	ACAGCATTTT	3960
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188	GGTTCCCAGA	CTAAGGGAAC	TAATATCTAT	ATAATTAAAC	TTGTTTCATTT	ATCATTCATG	4020
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190	AAATATAAAA	TACTTGTCAT	TTAAACCGTT	TAAAAATGTG	GTAGCATAAT	GTCACCCCAA	4080
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192	AAAGCATTCA	GAAAGCAATG	TAAGTGTGAA	GACCAGGGTT	TAAAGGTAAT	TCATTTATAG	4140
193							
194	TTTATAACTC	CTTAGATGTT	TGATGTTGAA	AACTGCTTTA	ACATGAAAAAT	TATCTTCCTC	4200
195							
196	TGCTCTGTGT	GAACAATAGC	TTTTAATTTA	AGATTGCTCA	CTACTGTACT	AGACTACTGG	4260
197							
198	TAGGTTTTTTT	TGGGGGGGGG	TGGGTAGGGA	TATGTGGGTA	ATGAAGCATT	TACTTACAGG	4320
199							
200	CTATCATACT	CTGAGGCCAA	TTTTATCTCC	AAAGCAATAA	TATCATTAAG	TGATTCACTT	4380
201							
202	CATAGAAGGC	TAAGTTTCTC	TAGGACAGAT	AGAAAAACATG	AATTTTGAAA	TATATAGAAC	4440
203							
204	AGTAGTTAAA	ATACTATATA	TTTCAACCCT	GGCTGGTAGA	TTGCTTATTT	TACTATCAGA	4500
205							

RAW SEQUENCE LISTING PATENT APPLICATION US/09/442,143

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206 AACTAAAAGA TAGATTTTTA CCAAACAGA AGTATCTGTA ATTTTATAA TTCATCAATT 4560
207
208 CTGGAATGCT ATATATAATA TTTAAAAGAC TTTTAAATG TGTTTAATTT CATCATCGTA 4620
209
210 AAAAGGGATC 4630
211

212 (2) INFORMATION FOR SEQ ID NO:2:
213

214 (i) SEQUENCE CHARACTERISTICS:

- 215 (A) LENGTH: 439 amino acids
- 216 (B) TYPE: amino acid
- 217 (C) STRANDEDNESS: single
- 218 (D) TOPOLOGY: linear

219
220 (ii) MOLECULE TYPE: peptide
221

222
223 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
224

225 Met Lys Leu Ala Asn Trp Tyr Trp Leu Ser Ser Ala Val Leu Ala Thr
226 1 5 10 15
227

228 Tyr Gly Phe Leu Val Val Ala Asn Asn Glu Thr Glu Glu Ile Lys Asp
229 20 25 30
230

231 Glu Arg Ala Lys Asp Val Cys Pro Val Arg Leu Glu Ser Arg Gly Lys
232 35 40 45
233

234 Cys Glu Glu Ala Gly Glu Cys Pro Tyr Gln Val Ser Leu Pro Pro Leu
235 50 55 60
236

237 Thr Ile Gln Leu Pro Lys Gln Phe Ser Arg Ile Glu Glu Val Phe Lys
238 65 70 75 80
239

240 Glu Val Gln Asn Leu Lys Glu Ile Val Asn Ser Leu Lys Lys Ser Cys
241 85 90 95
242

243 Gln Asp Cys Lys Leu Gln Ala Asp Asp Asn Gly Asp Pro Gly Arg Asn
244 100 105 110
245

246 Gly Leu Leu Leu Pro Ser Thr Gly Ala Pro Gly Glu Val Gly Asp Asn
247 115 120 125
248

249 Arg Val Arg Glu Leu Glu Ser Glu Val Asn Lys Leu Ser Ser Glu Leu
250 130 135 140
251

252 Lys Asn Ala Lys Glu Glu Ile Asn Val Leu His Gly Arg Leu Glu Lys
253 145 150 155 160
254

255 Leu Asn Leu Val Asn Met Asn Asn Ile Glu Asn Tyr Val Asp Ser Lys
256 165 170 175
257

258 Val Ala Asn Leu Thr Phe Val Val Asn Ser Leu Asp Gly Lys Cys Ser

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SEQUENCE VERIFICATION REPORT
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